

10/587956

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<110> Korea Research Institute of Bioscience and Biotechnology

<120> A novel Hansenula polymorpha gene coding for alpha 1,6 mannosyltransferase and process for the production of recombinant glycoproteins with Hansenula polymorpha mutant strain deficient in the same gene

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<170> KopatentIn 1.71

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<212> DNA

<213> Hansenula polymorpha

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gtg ctg aag cgc gcg cga ctc tac atg gcg acg aat cgc cgg ctg gtg 99
Val Leu Lys Arg Ala Arg Leu Tyr Met Ala Thr Asn Arg Arg Leu Val
15 20 25 30

gtt gtt ctt gtg gtg ctg ctg tac tgg gtg gtc cag aac gtt tgg acg 147
Val Val Leu Val Val Leu Leu Tyr Trp Val Val Gln Asn Val Trp Thr
35 40 45

tgg agc cct ggg acg cgc gat ttg gcc caa gtg gac gcg aag atc gag 195
Trp Ser Pro Gly Thr Arg Asp Leu Ala Gln Val Asp Ala Lys Ile Glu
50 55 60

gcc gag cta aac tcg aat cta cat act ttt gga gcg cat ttg cgc cac 243
Ala Glu Leu Asn Ser Asn Leu His Thr Phe Gly Ala His Leu Arg His
65 70 75

tta aac cgg ctt ccg gca gag tcg gcc acc ctg cgt gaa aaa ctc acc 291
Leu Asn Arg Leu Pro Ala Glu Ser Ala Thr Leu Arg Glu Lys Leu Thr
80 85 90

ttc tat ttc cca tat tat cct gaa aag ccc gtg ccg aac cag atc tgg 339
Phe Tyr Phe Pro Tyr Tyr Pro Glu Lys Pro Val Pro Asn Gln Ile Trp
95 100 105 110

cag aca tgg aag gtc gat ctc gaa gac gac aac ttc ccc aag cag tac 387
Gln Thr Trp Lys Val Asp Leu Glu Asp Asp Asn Phe Pro Lys Gln Tyr
115 120 125

aga cgg ttt cag aag acg tgg gtc gag aaa aat cca gac tac gtg tac 435
Arg Arg Phe Gln Lys Thr Trp Val Glu Lys Asn Pro Asp Tyr Val Tyr
130 135 140

cac ctg att ccg gac tct gtg att gag gac ttt gtg gcg agt ttg tac His Leu Ile Pro Asp Ser Val Ile Glu Asp Phe Val Ala Ser Leu Tyr 145 150 155	483
gcg aac gtg ccg gag gtg gtc aga gcg tac cag ctg ctt ccg aaa aat Ala Asn Val Pro Glu Val Val Arg Ala Tyr Gln Leu Leu Pro Lys Asn 160 165 170	531
atc atg aag gcg gat ttt ttc cgg tat ttg gtg atc tac gcg cgc gga Ile Met Lys Ala Asp Phe Phe Arg Tyr Leu Val Ile Tyr Ala Arg Gly 175 180 185 190	579
ggc acc tac tca gac atg gac acg gtg tgt tta aag ccg atc aag gac Gly Thr Tyr Ser Asp Met Asp Thr Val Cys Leu Lys Pro Ile Lys Asp 195 200 205	627
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ttc tcg cgc aga ctg cag ttc tgc cag tgg acg atc cag gcg aag ccg Phe Ser Arg Arg Leu Gln Phe Cys Gln Trp Thr Ile Gln Ala Lys Pro 255 260 265 270	819
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act ctg ttt gat tat ctg aac aat gtg gcg agc gac ggc aag ttg ggc Thr Leu Phe Asp Tyr Leu Asn Asn Val Ala Ser Asp Gly Lys Leu Gly 320 325 330	1011
gac ggg tac ggc gtg ggg tcg ttg tat tgg cgc aag cac ggc aaa tat Asp Gly Tyr Gly Val Gly Ser Leu Tyr Trp Arg Lys His Gly Lys Tyr 335 340 345 350	1059
aag ctg aaa aag aca gaa att aac aag aat aac gag cca ttg cat tct Lys Leu Lys Lys Thr Glu Ile Asn Lys Asn Asn Glu Pro Leu His Ser 355 360 365	1107
gag gac cag ctt atc aac tgg agg tcg ctg acc aac atg gac aag cca	1155

Glu Asp Gln Leu Ile Asn Trp Arg Ser Leu Thr Asn Met Asp Lys Pro
 370 375 380

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 Lys Ile Met Gly Asp Val Met Val Leu Pro Ile Thr Ser Phe Ser Pro
 385 390 395

aac gtg ggg cac atg ggc tca aag agc agc tca gat agg ctg gca ttt 1251
 Asn Val Gly His Met Gly Ser Lys Ser Ser Ser Asp Arg Leu Ala Phe
 400 405 410

gtg gag cat tta ttt tct ggc agc tgg aag cca aaa aac aaa taggaaa 1300
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 35 40 45

Pro Gly Thr Arg Asp Leu Ala Gln Val Asp Ala Lys Ile Glu Ala Glu
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Leu Asn Ser Asn Leu His Thr Phe Gly Ala His Leu Arg His Leu Asn
 65 70 75 80

Arg Leu Pro Ala Glu Ser Ala Thr Leu Arg Glu Lys Leu Thr Phe Tyr
 85 90 95

Phe Pro Tyr Tyr Pro Glu Lys Pro Val Pro Asn Gln Ile Trp Gln Thr
 100 105 110

Trp Lys Val Asp Leu Glu Asp Asp Asn Phe Pro Lys Gln Tyr Arg Arg
 115 120 125

Phe Gln Lys Thr Trp Val Glu Lys Asn Pro Asp Tyr Val Tyr His Leu
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Ile Pro Asp Ser Val Ile Glu Asp Phe Val Ala Ser Leu Tyr Ala Asn
 145 150 155 160

Val Pro Glu Val Val Arg Ala Tyr Gln Leu Leu Pro Lys Asn Ile Met
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Lys Ala Asp Phe Phe Arg Tyr Leu Val Ile Tyr Ala Arg Gly Gly Thr
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 Tyr Ser Asp Met Asp Thr Val Cys Leu Lys Pro Ile Lys Asp Trp Ala
 195 200 205
 Thr Phe Asp Arg Asp Leu Ile His Ala Ala Asp Asn Lys Ala Asp Leu
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 Ser Gln Ile Asp Pro Glu Ala Arg Thr Thr Pro Val Gly Leu Val Ile
 225 230 235 240
 Gly Ile Glu Ala Asp Pro Asp Arg Pro Asp Trp His Glu Trp Phe Ser
 245 250 255
 Arg Arg Leu Gln Phe Cys Gln Trp Thr Ile Gln Ala Lys Pro Gly His
 260 265 270
 Pro Leu Leu Arg Glu Leu Ile Ile Arg Ile Val Glu Glu Thr Phe Arg
 275 280 285
 Lys Gln His Met Gly Val Leu Lys Arg Val Glu Gly Lys Asp Ser Gly
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 Ala Asp Ile Met Gln Trp Thr Gly Pro Gly Ile Phe Thr Asp Thr Leu
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 Phe Asp Tyr Leu Asn Asn Val Ala Ser Asp Gly Lys Leu Gly Asp Gly
 325 330 335
 Tyr Gly Val Gly Ser Leu Tyr Trp Arg Lys His Gly Lys Tyr Lys Leu
 340 345 350
 Lys Lys Thr Glu Ile Asn Lys Asn Asn Glu Pro Leu His Ser Glu Asp
 355 360 365
 Gln Leu Ile Asn Trp Arg Ser Leu Thr Asn Met Asp Lys Pro Lys Ile
 370 375 380
 Met Gly Asp Val Met Val Leu Pro Ile Thr Ser Phe Ser Pro Asn Val
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cacccgcac 69